

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/635,130DATE: 08/01/96
TIME: 14:41:04

#5

INPUT SET: S11899.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

(1) General Information:

ENTERED

(i) APPLICANT: Caras, Ingrid W

(ii) TITLE OF INVENTION: A2-1 Neurotrophic Factor

(iii) NUMBER OF SEQUENCES: 8

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Genentech, Inc.

(B) STREET: 460 Point San Bruno Blvd

(C) CITY: South San Francisco

(D) STATE: California

(E) COUNTRY: USA

(F) ZIP: 94080

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: WinPatin (Genentech)

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 08/635130

(B) FILING DATE: 19-Mar-1996

(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Torchia, PhD., Timothy E.

(B) REGISTRATION NUMBER: 36,700

(C) REFERENCE/DOCKET NUMBER: P1001

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 415/225-8674

(B) TELEFAX: 415/952-9881

(C) TELEX: 910/371-7168

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1877 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

--> OK

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/635,130DATE: 08/01/96
TIME: 14:41:08

INPUT SET: S11899.raw

47
48 (ix) FEATURE:
49 (A) NAME/KEY: Extra Cellular Domain
50 (B) LOCATION: 244-899
51 (C) IDENTIFICATION METHOD:
52 (D) OTHER INFORMATION:
53
54 (ix) FEATURE:
55 (A) NAME/KEY: Transmembrane Domain
56 (B) LOCATION: 901-978
57 (C) IDENTIFICATION METHOD:
58 (D) OTHER INFORMATION:
59
60 (ix) FEATURE:
61 (A) NAME/KEY: signal peptide
62 (B) LOCATION: 244-321
63 (C) IDENTIFICATION METHOD:
64 (D) OTHER INFORMATION:
65
66 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
67
68
69 GNTCTAGAAN TAGTGGATCC CCCCAGGCTG CAGGAATTCC GACGGCCCCT 50
70
71 GGAAGGGCTC TGGTGGGGCT GAGCGCTCTG CCGCGGGGGC GCGGGCACAG 100
72
73 CAGGAAGCAG GTCCGCGTGG GCGCTGGGGG CATCAGCTAC CGGGGTGGTC 150
74
75 CGGGCTGAAG AGCCAGGCAG CCAAGGCAGC CACCCCGGGG GGTGGGCGAC 200
76
77 TTTGGGGGAG TTGGTGCCCC GCCCCCAGG CCTTGGCGGG GTC ATG 246
78 Met
79 1
80
81 GGG CCC CCC CAT TCT GGG CCG GGG GGC GTG CGA GTC GGG 285
82 Gly Pro Pro His Ser Gly Pro Gly Gly Val Arg Val Gly
83 5 10
84
85 GCC CTG CTG CTG CTG GGG GTT TTG GGG CTG GTG TCT GGG 324
86 Ala Leu Leu Leu Leu Gly Val Leu Gly Leu Val Ser Gly
87 15 20 25
88
89 CTC AGC CTG GAG CCT GTC TAC TGG AAC TCG GCG AAT AAG 363
90 Leu Ser Leu Glu Pro Val Tyr Trp Asn Ser Ala Asn Lys
91 30 35 40
92
93 AGG TTC CAG GCA GAG GGT GGT TAT GTG CTG TAC CCT CAG 402
94 Arg Phe Gln Ala Glu Gly Gly Tyr Val Leu Tyr Pro Gln
95 45 50
96
97 ATC GGG GAC CGG CTA GAC CTG CTC TGC CCC CGG GCC CGG 441
98 Ile Gly Asp Arg Leu Asp Leu Leu Cys Pro Arg Ala Arg
99 55 60 65

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100														
101	CCT	CCT	GGC	CCT	CAC	TCC	TCT	CCT	AAT	TAT	GAG	TTC	TAC	480
102	Pro	Pro	Gly	Pro	His	Ser	Ser	Pro	Asn	Tyr	Glu	Phe	Tyr	
103				70					75					
104														
105	AAG	CTG	TAC	CTG	GTA	GGG	GGT	GCT	CAG	GGC	CGG	CGC	TGT	519
106	Lys	Leu	Tyr	Leu	Val	Gly	Gly	Ala	Gln	Gly	Arg	Arg	Cys	
107	80					85					90			
108														
109	GAG	GCA	CCC	CCT	GCC	CCA	AAC	CTC	CTT	CTC	ACT	TGT	GAT	558
110	Glu	Ala	Pro	Pro	Ala	Pro	Asn	Leu	Leu	Leu	Thr	Cys	Asp	
111			95					100					105	
112														
113	CGC	CCA	GAC	CTG	GAT	CTC	CGC	TTC	ACC	ATC	AAG	TTC	CAG	597
114	Arg	Pro	Asp	Leu	Asp	Leu	Arg	Phe	Thr	Ile	Lys	Phe	Gln	
115					110					115				
116														
117	GAG	TAT	AGC	CCT	AAT	CTC	TGG	GGC	CAC	GAG	TTC	CGC	TCG	636
118	Glu	Tyr	Ser	Pro	Asn	Leu	Trp	Gly	His	Glu	Phe	Arg	Ser	
119		120					125					130		
120														
121	CAC	CAC	GAT	TAC	TAC	ATC	ATT	GCC	ACA	TCG	GAT	GGG	ACC	675
122	His	His	Asp	Tyr	Tyr	Ile	Ile	Ala	Thr	Ser	Asp	Gly	Thr	
123				135					140					
124														
125	CGG	GAG	GGC	CTG	GAG	AGC	CTG	CAG	GGA	GGT	GTG	TGC	CTA	714
126	Arg	Glu	Gly	Leu	Glu	Ser	Leu	Gln	Gly	Gly	Val	Cys	Leu	
127	145					150					155			
128														
129	ACC	AGA	GGC	ATG	AAG	GTG	CTT	CTC	CGA	GTG	GGA	CAA	AGT	753
130	Thr	Arg	Gly	Met	Lys	Val	Leu	Leu	Arg	Val	Gly	Gln	Ser	
131			160					165					170	
132														
133	CCC	CGA	GGA	GGG	GCT	GTC	CCC	CGA	AAA	CCT	GTG	TCT	GAA	792
134	Pro	Arg	Gly	Gly	Ala	Val	Pro	Arg	Lys	Pro	Val	Ser	Glu	
135					175					180				
136														
137	ATG	CCC	ATG	GAA	AGA	GAC	CGA	GGG	GCA	GCC	CAC	AGC	CTG	831
138	Met	Pro	Met	Glu	Arg	Asp	Arg	Gly	Ala	Ala	His	Ser	Leu	
139		185					190					195		
140														
141	GAG	CCT	GGG	AAG	GAG	AAC	CTG	CCA	GGT	GAC	CCC	ACC	AGC	870
142	Glu	Pro	Gly	Lys	Glu	Asn	Leu	Pro	Gly	Asp	Pro	Thr	Ser	
143				200					205					
144														
145	AAT	GCA	ACC	TCC	CGG	GGT	GCT	GAA	GGC	CCC	CTG	CCC	CCT	909
146	Asn	Ala	Thr	Ser	Arg	Gly	Ala	Glu	Gly					

RAW SEQUENCE LISTING PATENT APPLICATION US/08/635,130

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TIME: 14:41:15

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153   GCG CTG CTC TTG CTG GGC GTG GCA GGG GCT GGG GGT GCC 987
154   Ala Leu Leu Leu Leu Gly Val Ala Gly Ala Gly Gly Ala
155           240           245
156
157   ATG TGT TGG CGG AGA CGG CGG GCC AAG CCT TCG GAG AGT 1026
158   Met Cys Trp Arg Arg Arg Arg Ala Lys Pro Ser Glu Ser
159           250           255           260
160
161   CGC CAC CCT GGT CCT GGC TCC TTC GGG AGG GGA GGG TCT 1065
162   Arg His Pro Gly Pro Gly Ser Phe Gly Arg Gly Gly Ser
163           265           270
164
165   CTG GGC CTG GGG GGT GGA GGT GGG ATG GGA CCT CGG GAG 1104
166   Leu Gly Leu Gly Gly Gly Gly Gly Met Gly Pro Arg Glu
167   275           280           285
168
169   GCT GAG CCT GGG GAG CTA GGG ATA GCT CTG CGG GGT GGC 1143
170   Ala Glu Pro Gly Glu Leu Gly Ile Ala Leu Arg Gly Gly
171           290           295           300
172
173   GGG GCT GCA GAT CCC CCC TTC TGC CCC CAC TAT GAG AAG 1182
174   Gly Ala Ala Asp Pro Pro Phe Cys Pro His Tyr Glu Lys
175           305           310
176
177   GTG AGT GGT GAC TAT GGG CAT CCT GTG TAT ATC GTG CAG 1221
178   Val Ser Gly Asp Tyr Gly His Pro Val Tyr Ile Val Gln
179           315           320           325
180
181   GAT GGG CCC CCC CAG AGC CCT CCA AAC ATC TAC TAC ACA 1260
182   Asp Gly Pro Pro Gln Ser Pro Pro Asn Ile Tyr Tyr Thr
183           330           335
184
185   TCG ATT TCT GTG TTG GAG TGG CCC ATA TTG CAT ACG ATA 1299
186   Ser Ile Ser Val Leu Glu Trp Pro Ile Leu His Thr Ile
187   340           345           350
188
189   CAA CTG TTT TTC ATG CGA TCC AAG TGC TCC CGT GTC ACT 1338
190   Gln Leu Phe Phe Met Arg Ser Lys Cys Ser Arg Val Thr
191           355           360           365
192
193   ACA TTC TTA TTT CCT GTG CAA GTT ATT ACG ACA TCG ACT 1377
194   Thr Phe Leu Phe Pro Val Gln Val Ile Thr Thr Ser Thr
195           370           375
196
197   TGC CGG ATG ACT TCA TTT AGC TTT ACC ACC CTG AAC CCA 1416
198   Cys Arg Met Thr Ser Phe Ser Phe Thr Thr Leu Asn Pro
199           380           385           390
200
201   TCC ATG CAG GCC TGC AGA GCA CAG ATG GGG GAA TTC CGA 1455
202   Ser Met Gln Ala Cys Arg Ala Gln Met Gly Glu Phe Arg
203           395           400
204
205   ATC AGA TGG TGT TTC TGG GGG GAC AGG ATC CTG GGT ACG 1494

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INPUT SET: S11899.raw

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206 Ile Arg Trp Cys Phe Trp Gly Asp Arg Ile Leu Gly Thr
207 405 410 415
208
209 GCT CTG TTT GTG CTT GTG CTT ATT CTT CTT CTT GGG AGG 1533
210 Ala Leu Phe Val Leu Val Leu Ile Leu Leu Leu Gly Arg
211 420 425 430
212
213 CTG AAT ATG CAT CAG ACG ACA CTG CTC CGG CAA CGG GCC 1572
214 Leu Asn Met His Gln Thr Thr Leu Leu Arg Gln Arg Ala
215 435 440
216
217 AGT GTG GAG GCG GAA GCC GGC CAG CAT GGT CCC CTG TG 1610
218 Ser Val Glu Ala Glu Ala Gly Gln His Gly Pro Leu
219 445 450 455
220
221 ATAGGATTGA AAGAGCTACT GAGAATAGGG GGCTTCTCAA TGAGAGAGCG 1660
222
223 GAGGCTGCTG TTATCATGGG AACCAGGCAG ATCAATCATC CCTGGCAGGT 1710
224
225 CAGGCAGGAA GTTACTTAGC TTCTCCTTCA CCTTCTTCCC ACAGAATTTA 1760
226
227 TTATAGGCTT GTTCCAAGTT GTAGTGTGTG ATCAGATTCG TGCTGCCTGT 1810
228
229 CAGCTCTGTG CTACCTGGCA GTTCCCCTCA TGGAATTCGA TATCAAGCTT 1860
230
231 ATCGATAACCG TCGACCT 1877
232
233 (2) INFORMATION FOR SEQ ID NO:2:
234
235 (i) SEQUENCE CHARACTERISTICS:
236 (A) LENGTH: 455 amino acids
237 (B) TYPE: Amino Acid
238 (D) TOPOLOGY: Linear
239
240 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
241
242 Met Gly Pro Pro His Ser Gly Pro Gly Gly Val Arg Val Gly Ala
243 1 5 10 15
244
245 Leu Leu Leu Leu Gly Val Leu Gly Leu Val Ser Gly Leu Ser Leu
246 20 25 30
247
248 Glu Pro Val Tyr Trp Asn Ser Ala Asn Lys Arg Phe Gln Ala Glu
249 35 40 45
250
251 Gly Gly Tyr Val Leu Tyr Pro Gln Ile Gly Asp Arg Leu Asp Leu
252 50 55 60
253
254 Leu Cys Pro Arg Ala Arg Pro Pro Gly Pro His Ser Ser Pro Asn
255 65 70 75
256
257 Tyr Glu Phe Tyr Lys Leu Tyr Leu Val Gly Gly Ala Gln Gly Arg
258 80 85 90

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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/08/635,130

DATE: 08/01/96
TIME: 14:41:22

INPUT SET: S11899.raw

Line	Error	Original Text
26	Wrong application Serial Number	(A) APPLICATION NUMBER: 08/635130